

## REMARKS

The specification and claims have been amended to delete any reference to SEQ. ID. NO: 1. SEQ. ID. NO: 1 is not an essential or even important element of the invention. SEQ. ID. NO: 1, as set forth in the specification referred to a sequence determined of the 16S rRNA gene. This can be used as a taxonomic tool. As the organism of the invention has been deposited and defined by other characteristics as set forth in the specification, this taxonomic tool is unnecessary to the invention.

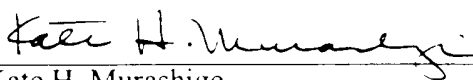
It was noticed, in reviewing the claims, that fees were paid only for a total of 42 claims; however, multiple dependencies expands the actual number of claims to a greater number. To correct this, multiple dependencies have been eliminated. It is noted that additional filing fees were authorized to be deducted from the deposit account of the original representative; however, it is not clear whether this was in fact done. In addition, claims 23-42 directed to compositions have been replaced by claims directed to methods. These methods are supported, for example, on page 14, beginning at line 11. No new matter has been added and entry of the amendment is respectfully requested.

In the unlikely event that the transmittal letter is separated from this document and the Patent Office determines that an extension and/or other relief is required, applicants petition for any required relief including extensions of time and authorize the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to **Deposit Account No. 03-1952** referencing docket No. 524182000400.

Respectfully submitted,

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By:

  
Kate H. Murashige  
Registration No. 29,959

Morrison & Foerster <sup>L.L.P.</sup>  
3811 Valley Centre Drive, Suite 500  
San Diego, California 92130-2332  
Telephone: (858) 720-5112  
Facsimile: (858) 720-5125

## EXHIBIT A. - VERSION WITH MARKINGS TO SHOW CHANGES MADE

### In the Specification:

Please amend the paragraph at page 28, lines 9-24, as follows:

The next logical step was to determine the 16S rRNA gene sequence. This technique currently is the method of choice for identification purposes. [The gene sequence is shown in SEQ ID NO: 1.] The identification based on the 16S rRNA gene sequence was determined to be *Leclercia adecarboxylata*. The difference in sequence homology between LAB-1 and *L. adecarboxylata* was only 0.59%. Stackebrandt & Goebel, INT'L J. SYSTEM. BACTERIOL. 44: 846 (1994) would consider this a species level match, however the confidence limits of the data obtained by MIDI LABS™ allowed identification only at the genus level. When the biochemical characteristics of LAB-1 and of *L. adecarboxylata* (9<sup>th</sup> edition Bergey's Manual of Determinative Bacteriology 1994) are compared, there are yet again, numerous differences. The differences led to the questions regarding this method.

### In the Claims:

11. (Amended) An exopolysaccharide produced by the bacterium of [claims 1-8] claim 1.

17. (Amended) The biofilm of claim 16, which is produced by the bacterium of [claims 1-8] claim 1.

20. (Amended) The plasma expander of claim 18, wherein the exopolysaccharide is produced by the bacterium of [claims 1-8] claim 1.